



PCT10

RAW SEQUENCE LISTING

DATE: 04/17/2002

PATENT APPLICATION: US/10/089,485

TIME: 12:16:40

Input Set : A:\62489.txt

Output Set: N:\CRF3\04172002\J089485.raw

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3 <110> APPLICANT: Hanada and Yang
5 <120> TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR-5 (FGF-5) IS A TUMOR
6   ASSOCIATED T-CELL ANTIGEN
8 <130> FILE REFERENCE: 55911
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/089,485
C--> 11 <141> CURRENT FILING DATE: 2002-03-27
13 <150> PRIOR APPLICATION NUMBER: PCT/US00/26689
14 <151> PRIOR FILING DATE: 2000-09-29
16 <150> PRIOR APPLICATION NUMBER: 60/157,103
17 <151> PRIOR FILING DATE: 1999-10-02
19 <160> NUMBER OF SEQ ID NOS: 25
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 143
25 <212> TYPE: DNA
26 <213> ORGANISM: Homo sapiens
28 <220> FEATURE:
29 <221> NAME/KEY: CDS
30 <222> LOCATION: (27)..(140)
32 <400> SEQUENCE: 1
33 cctctccccc tctcttcccc gaggct atg tcc acc cgg tgc ggc gag gcg ggc 53
34                               Met Ser Thr Arg Cys Gly Glu Ala Gly
35                               1           5
37 aga gcc aga ggc acg cag ccg cac agg ggc tac aga gcc cag aat caa 101
38 Arg Ala Arg Gly Thr Gln Pro His Arg Gly Tyr Arg Ala Gln As
39 10           15           20
41 ccc tac aag atg cac tta gga ccc ccg cgg ctg gaa gaa tga 143
42 Pro Tyr Lys Met His Leu Gly Pro Pro Arg Leu Glu Glu
43           30           35
46 <210> SEQ ID NO: 2
47 <211> LENGTH: 38
48 <212> TYPE: PRT
49 <213> ORGANISM: Homo sapiens
51 <400> SEQUENCE: 2
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53 1           5           10           15
55 His Arg Gly Tyr Arg Ala Gln Asn Gln Pro Tyr Lys Met His Leu Gly
56           20           25           30
58 Pro Pro Arg Leu Glu Glu
59           35
63 <210> SEQ ID NO: 3
64 <211> LENGTH: 1123
65 <212> TYPE: DNA

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66 <213> ORGANISM: Homo sapiens

68 <220> FEATURE:

69 <221> NAME/KEY: CDS

70 <222> LOCATION: (140)..(946)

72 <400> SEQUENCE: 3

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73 cctctccctt tctcttcccc gaggtatgt ccacccggtg cggcgaggcg ggcagagcca 60
75 gaggcacgca gccgcacagg ggctacagag ccagaaatca gccctacaag atgcacttag 120
77 gacccccgcg gctggaaga atg agc ttg tcc ttc ctc ctc ctc ctc ttc ttc 172
78                               Met Ser Leu Ser Phe Leu Leu Leu Leu Phe Phe
79                               1             5             10
81 agc cac ctg atc ctc agc gcc tgg gct cac ggg gag aag cgt ctc gcc 220
82 Ser His Leu Ile Leu Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala
83                               15             20             25
85 ccc aaa ggg caa ccc gga ccc gct gcc act gat agg aac cct ata ggc 268
86 Pro Lys Gly Gln Pro Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly
87                               30             35             40
89 tcc agc agc aga cag agc agc agt agc gct atg tct tcc tct tct gcc 316
90 Ser Ser Ser Arg Gln Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala
91                               45             50             55
93 tcc tcc tcc ccc gca gct tct ctg ggc agc caa gga agt ggc ttg gag 364
94 Ser Ser Ser Pro Ala Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu
95 60                               65             70             75
97 cag agc agt ttc cag tgg agc ccc tcg ggg cgc cgg acc ggc agc ctc 412
98 Gln Ser Ser Phe Gln Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu
99                               80             85             90
101 tac tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc 460
102 Tyr Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly
103                               95             100             105
105 aaa gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata 508
106 Lys Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile
107                               110             115             120
109 ttt gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac 556
110 Phe Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn
111                               125             130             135
113 aaa ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag 604
114 Lys Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys
115 140                               145             150             155
117 ttc aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat 652
118 Phe Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr
119                               160             165             170
121 aat acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag 700
122 Asn Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu
123                               175             180             185
125 tgg tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc 748
126 Trp Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser
127                               190             195             200
129 ccc cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc 796
130 Pro Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe
131                               205             210             215

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133 aag cag tcg gag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa      844
134 Lys Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu
135 220                      225                      230                      235
137 aag aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca      892
138 Lys Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala
139                      240                      245                      250
141 cct cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt      940
142 Pro Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe
143                      255                      260                      265
145 gga taa tattaatctt ggcccttgta gaaaccattc tttccctca ggagtttcta      996
146 Gly
148 taggtgtctt cagagttctg aagaaaaatt actggacaca gcttcagcta tacttacact 1056
150 gtattgaagt caggtcattt gtttcagtgt gactgaaaca aaatgttttt tgataggaag 1116
152 gaaactg                                     1123
155 <210> SEQ ID NO: 4
156 <211> LENGTH: 268
157 <212> TYPE: PRT
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 4
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162 1                      5                      10                      15
163 Ser Ala Trp Ala His Gly Glu Lys Arg Leu Ala Pro Lys Gly Gln Pro
164                      20                      25                      30
165 Gly Pro Ala Ala Thr Asp Arg Asn Pro Ile Gly Ser Ser Ser Arg Gln
166                      35                      40                      45
167 Ser Ser Ser Ser Ala Met Ser Ser Ser Ser Ala Ser Ser Ser Pro Ala
168                      50                      55                      60
169 Ala Ser Leu Gly Ser Gln Gly Ser Gly Leu Glu Gln Ser Ser Phe Gln
170 65                      70                      75                      80
171 Trp Ser Pro Ser Gly Arg Arg Thr Gly Ser Leu Tyr Cys Arg Val Gly
172                      85                      90                      95
173 Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys Val Asn Gly Ser
174                      100                     105                     110
175 His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe Ala Val Ser Gln
176                      115                     120                     125
177 Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys Phe Leu Ala Met
178                      130                     135                     140
179 Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe Thr Asp Asp Cys
180 145                      150                     155                     160
181 Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn Thr Tyr Ala Ser
182                      165                     170                     175
183 Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp Tyr Val Ala Leu
184                      180                     185                     190
185 Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro Arg Val Lys Pro
186                      195                     200                     205
187 Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys Gln Ser Glu Gln
188                      210                     215                     220
189 Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys Lys Asn Pro Pro
190 225                      230                     235                     240

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191 Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro Arg Lys Asn Thr
192                245                250                255
193 Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
194                260                265
198 <210> SEQ ID NO: 5
199 <211> LENGTH: 531
200 <212> TYPE: DNA
201 <213> ORGANISM: Homo sapiens
203 <220> FEATURE:
204 <221> NAME/KEY: CDS
205 <222> LOCATION: (1)..(531)
207 <400> SEQUENCE: 5
208 tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc aaa      48
209 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
210 1          5          10          15
212 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt      96
213 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
214                20                25                30
216 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa      144
217 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
218                35                40                45
220 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc      192
221 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
222                50                55                60
224 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat      240
225 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
226 65          70          75          80
228 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg      288
229 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
230                85                90                95
232 tat gtt gcc ctg aat aaa aga gga aaa gcc aaa cga ggg tgc agc ccc      336
233 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
234                100               105               110
236 cgg gtt aaa ccc cag cat atc tct acc cat ttt ctt cca aga ttc aag      384
237 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
238                115               120               125
240 cag tcg gag cag cca gaa ctt tct ttc acg gtt act gtt cct gaa aag      432
241 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
242                130               135               140
244 aaa aat cca cct agc cct atc aag tca aag att ccc ctt tct gca cct      480
245 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
246 145          150          155          160
248 cgg aaa aat acc aac tca gtg aaa tac aga ctc aag ttt cgc ttt gga      528
249 Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
250                165               170               175
252 taa      531
256 <210> SEQ ID NO: 6
257 <211> LENGTH: 176
258 <212> TYPE: PRT

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259 <213> ORGANISM: Homo sapiens
261 <400> SEQUENCE: 6
262 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
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264 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
265           20           25           30
266 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
267   35           40           45
268 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
269   50           55           60
270 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
271  65           70           75           80
272 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp
273           85           90           95
274 Tyr Val Ala Leu Asn Lys Arg Gly Lys Ala Lys Arg Gly Cys Ser Pro
275           100          105          110
276 Arg Val Lys Pro Gln His Ile Ser Thr His Phe Leu Pro Arg Phe Lys
277           115          120          125
278 Gln Ser Glu Gln Pro Glu Leu Ser Phe Thr Val Thr Val Pro Glu Lys
279           130          135          140
280 Lys Asn Pro Pro Ser Pro Ile Lys Ser Lys Ile Pro Leu Ser Ala Pro
281 145           150          155          160
282 Arg Lys Asn Thr Asn Ser Val Lys Tyr Arg Leu Lys Phe Arg Phe Gly
283           165          170          175
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 531
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(531)
296 <400> SEQUENCE: 7
297 tgc aga gtg ggc atc ggt ttc cat ctg cag atc tac ccg gat ggc aaa 48
298 Cys Arg Val Gly Ile Gly Phe His Leu Gln Ile Tyr Pro Asp Gly Lys
299   1           5           10           15
301 gtc aat gga tcc cac gaa gcc aat atg tta agt gtt ttg gaa ata ttt 96
302 Val Asn Gly Ser His Glu Ala Asn Met Leu Ser Val Leu Glu Ile Phe
303           20           25           30
305 gct gtg tct cag ggg att gta gga ata cga gga gtt ttc agc aac aaa 144
306 Ala Val Ser Gln Gly Ile Val Gly Ile Arg Gly Val Phe Ser Asn Lys
307           35           40           45
309 ttt tta gcg atg tca aaa aaa gga aaa ctc cat gca agt gcc aag ttc 192
310 Phe Leu Ala Met Ser Lys Lys Gly Lys Leu His Ala Ser Ala Lys Phe
311           50           55           60
313 aca gat gac tgc aag ttc agg gag cgt ttt caa gaa aat agc tat aat 240
314 Thr Asp Asp Cys Lys Phe Arg Glu Arg Phe Gln Glu Asn Ser Tyr Asn
315  65           70           75           80
317 acc tat gcc tca gca ata cat aga act gaa aaa aca ggg cgg gag tgg 288
318 Thr Tyr Ala Ser Ala Ile His Arg Thr Glu Lys Thr Gly Arg Glu Trp

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VERIFICATION SUMMARY

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Input Set : A:\62489.txt

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L:10 M:270 C: Current Application Number differs, Replaced Application Number
L:11 M 271 C: Current Filing Date differs, Replaced Current Filing Date